

Plant genes contribute to a sexually transmitted disease? How plant genes found their way into a human parasite

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The most frequently reported sexually transmitted disease in the United States is caused by the parasitic bacterium *Chlamydia trachomatis*. Although about half a million cases of infection are reported annually, a more realistic incidence is around 4 million cases per year. This is because there is a large pool of asymptomatic individuals within the population. If left untreated, chlamydial infections can develop into pelvic inflammatory disease (PID) and can also cause severe but curable eye disease (trachoma).

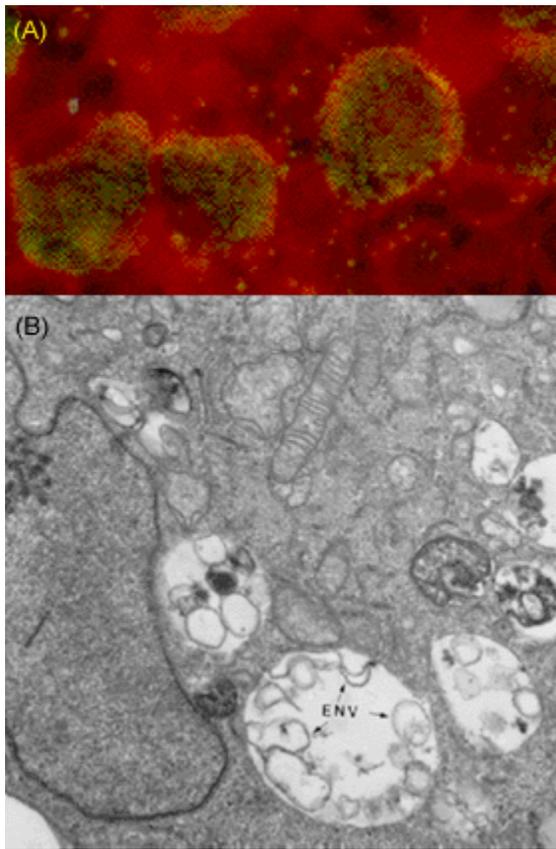
The Chlamydia Genome Project consortium has recently sequenced the *C. trachomatis* genome. It has a circular chromosome of about 1,045,000 base pairs, about one-quarter the size of *Escherichia coli*. Analysis of the sequence has identified 888 protein-coding genes. Among these, some proteins appear to have an unconventional natural history.

The genome appears to have undergone an unusually high number of horizontal gene transfer events, suggesting that the parasitic nature of *C. trachomatis* provides greater opportunity for gene transfer to occur. More bizarre, though, is that some of the *C. trachomatis* proteins are more related to green plants than to other bacteria or their human hosts. FabI and FabF, two chlamydial proteins involved in the fatty acid synthesis component of membrane biogenesis, seem to be most closely related to their

plant counterparts, whereas plsB, involved in lipopolysaccharide biosynthesis, has only plant orthologs.

How this came to be relies on linking two pieces of information. First, a *Chlamydia*-like parasite has been found recently in *Acanthamoeba*, a free-living protozoan usually found in fresh water or soil but which may occur as a human pathogen. Perhaps *Acanthamoeba* represents the original host for *Chlamydia*, and served as a vector to transfer its *Chlamydia* parasite to humans. Second, inferences made from 16S-like RNA provide evidence that *Acanthamoeba* is phylogenetically related to green plants. One would therefore expect some *Acanthamoeba* and green plant genes to be highly related. Horizontal transfer between *Acanthamoeba* (host) and *Chlamydia* (parasite) could therefore give plant-like genes to *Chlamydia*. If this horizontal transfer occurred before *Chlamydia* was passed to humans, then it is possible that a human parasite has plant-like genes.

Analysis of the genome of *Chlamydia* will provide a starting point for a deeper understanding of other eukaryotic parasites, including those responsible for human disease.



***Chlamydia trachomatis* inclusions in infected cells** *Chlamydia trachomatis* inclusions in infected human genital epithelial cells.

(A) The inclusions are seen as green or yellow spots by fluorescence photomicroscopy. (Photograph by Stephen T. Knight.)

(B) Inside a *Chlamydia trachomatis*-infected human genital epithelial cell. If the cells are exposed to the antibiotic azithromycin, the viable *Chlamydia* are killed, leaving residual chlamydial envelope material ("ENV"; one of these vesicles is equivalent to one of the yellow/green spots in (A) above, at this much higher magnification). (Photograph by Jane E. Raulston.)

Both photographs are from studies at the *Chlamydia* laboratories of Drs P. B. Wyrick and J. E. Raulson, Dept of Microbiology and Immunology, University of North Carolina School of Medicine, Chapel Hill, NC 7290, USA.

Box: Search PubMed for chlamydia adapting to live in human cells

Click the link below to start an html tutorial.

How has chlamydia adapted to live in human cells? [http://www.ncbi.nlm.nih.gov/Coffeebreak/CB1_Chlamydia/PQ1.html]

Box: Search PubMed for horizontal gene transfer

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Horizontal gene transfer in pathogenesis [http://www.ncbi.nlm.nih.gov/Coffeebreak/CB1_Chlamydia/PQ2.html]

Box: Use BLAST to search for chlamydia fatty acid synthesis enzymes

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Chlamydia fatty acid synthesis enzymes match plant enzyme sequences [http://www.ncbi.nlm.nih.gov/Coffeebreak/CB1_Chlamydia/BQ.html]